

1. The following table shows the number of people who have been convicted of a crime in the United States since 1970.	
Year	Number of people convicted
1970	100,000
1971	105,000
1972	110,000
1973	115,000
1974	120,000
1975	125,000
1976	130,000
1977	135,000
1978	140,000
1979	145,000
1980	150,000
1981	155,000
1982	160,000
1983	165,000
1984	170,000
1985	175,000
1986	180,000
1987	185,000
1988	190,000
1989	195,000
1990	200,000
1991	205,000
1992	210,000
1993	215,000
1994	220,000
1995	225,000
1996	230,000
1997	235,000
1998	240,000
1999	245,000
2000	250,000
2001	255,000
2002	260,000
2003	265,000
2004	270,000
2005	275,000
2006	280,000
2007	285,000
2008	290,000
2009	295,000
2010	300,000
2011	305,000
2012	310,000
2013	315,000
2014	320,000
2015	325,000
2016	330,000
2017	335,000
2018	340,000
2019	345,000
2020	350,000
2021	355,000
2022	360,000
2023	365,000
2024	370,000
2025	375,000
2026	380,000
2027	385,000
2028	390,000
2029	395,000
2030	400,000
2031	405,000
2032	410,000
2033	415,000
2034	420,000
2035	425,000
2036	430,000
2037	435,000
2038	440,000
2039	445,000
2040	450,000
2041	455,000
2042	460,000
2043	465,000
2044	470,000
2045	475,000
2046	480,000
2047	485,000
2048	490,000
2049	495,000
2050	500,000
2051	505,000
2052	510,000
2053	515,000
2054	520,000
2055	525,000
2056	530,000
2057	535,000
2058	540,000
2059	545,000
2060	550,000
2061	555,000
2062	560,000
2063	565,000
2064	570,000
2065	575,000
2066	580,000
2067	585,000
2068	590,000
2069	595,000
2070	600,000
2071	605,000
2072	610,000
2073	615,000
2074	620,000
2075	625,000
2076	630,000
2077	635,000
2078	640,000
2079	645,000
2080	650,000
2081	655,000
2082	660,000
2083	665,000
2084	670,000
2085	675,000
2086	680,000
2087	685,000
2088	690,000
2089	695,000
2090	700,000
2091	705,000
2092	710,000
2093	715,000
2094	720,000
2095	725,000
2096	730,000
2097	735,000
2098	740,000
2099	745,000
2100	750,000

<120> Adenovirus particles with mutagenized fiber proteins

<160> 43

 $\langle 210 \rangle$ 1

<212> DNA

<213> Human adenovirus type 5

 $\langle 220 \rangle$

<221> CDS

<222> (1) .. (1746)

 $\langle 400 \rangle$ 1

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

```

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc      2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65              70              75              80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac      2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85              90              95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta      3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100              105              110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc      3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115              120              125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att      4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130              135              140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa      4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145              150              155              160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act      5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

```

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8
16

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
64

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

4-31452A.ST25.txt

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
 12
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
 60
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305

310

315

320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
 08
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
 56
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
 04
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
 52
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
 00

4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405 410 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420 425 430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435 440 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13
92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450 455 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14
88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15

4-31452A.ST25.txt

Met	Lys	Arg	Ala	Arg	Pro	Ser	Glu	Asp	Thr	Phe	Asn	Pro	Val	Tyr	Pro	
1				5					10					15		
Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro	
			20					25					30			
Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser	
		35					40					45				
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu	
	50					55					60					
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser	
65					70					75					80	
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn	
				85					90					95		
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu	
			100					105					110			
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr	
		115					120					125				
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile	
	130					135					140					
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln	
145					150					155					160	
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr	
				165					170					175		
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu	
			180					185					190			

4-31452A.ST25.txt

Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly			
		195					200					205						
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr			
	210					215					220							
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr			
225					230					235					240			
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala			
				245					250					255				
Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val			
			260					265					270					
Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln			
		275					280					285						
Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn			
	290					295					300							
Lys	Gly	Leu	Tyr	Leu	Phe	Thr	Ala	Ser	Asn	Asn	Ser	Lys	Lys	Leu	Glu			
305					310					315					320			
Val	Asn	Leu	Ser	Thr	Ala	Lys	Gly	Leu	Met	Phe	Asp	Ala	Thr	Ala	Ile			
				325					330					335				
Ala	Ile	Asn	Ala	Gly	Asp	Gly	Leu	Glu	Phe	Gly	Ser	Pro	Asn	Ala	Pro			
			340					345					350					
Asn	Thr	Asn	Pro	Leu	Lys	Thr	Lys	Ile	Gly	His	Gly	Leu	Glu	Phe	Asp			
		355					360					365						
Ser	Asn	Lys	Ala	Met	Val	Pro	Lys	Leu	Gly	Thr	Gly	Leu	Ser	Phe	Asp			
	370					375					380							

4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

Tyr Ile Ala Gln Glu
580

<210> 3

<211> 1746

<212> DNA

<213> Artificial

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>

<221> CDS

<222> (1)..(1746)

<220>

<221> mutation

<222> (1222)..(1227)

<400> 3

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

aaa 40	atg	ggc	aac	ggc	ctc	tct	ctg	gac	gag	gcc	ggc	aac	ctt	acc	tcc	2
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser	
65					70					75					80	
caa 88	aat	gta	acc	act	gtg	agc	cca	cct	ctc	aaa	aaa	acc	aag	tca	aac	2
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn	
				85					90					95		
ata 36	aac	ctg	gaa	ata	tct	gca	ccc	ctc	aca	gtt	acc	tca	gaa	gcc	cta	3
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu	
			100					105					110			
act 84	gtg	gct	gcc	gcc	gca	cct	cta	atg	gtc	gcg	ggc	aac	aca	ctc	acc	3
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr	
		115					120					125				
atg 32	caa	tca	cag	gcc	ccg	cta	acc	gtg	cac	gac	tcc	aaa	ctt	agc	att	4
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile	
	130					135					140					
gcc 80	acc	caa	gga	ccc	ctc	aca	gtg	tca	gaa	gga	aag	cta	gcc	ctg	caa	4
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln	
145					150					155					160	
aca 28	tca	ggc	ccc	ctc	acc	acc	acc	gat	agc	agt	acc	ctt	act	atc	act	5
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr	

175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

285

290 295 300

305 310 315 320

325 330 335

340 345 350

355 360 365

370 375 380

00

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

510

15

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

525

16

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

540

16

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

560

17

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

575

17

Tyr Ile Ala Gln Glu

580

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<210> 4
<211> 581
<212> PRT
<213> Artificial
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<400> 4

4-31452A.ST25.txt

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Tyr Ile Ala Gln Glu
580

<210> 5
<211> 1740
<212> DNA
<213> Artificial

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 441(V) & 442(K) of wild-type fiber were deleted

<220>
<221> CDS
<222> (1)..(1740)

<400> 5
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1
92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
 40
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80

 caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
 88
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95

 ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
 36
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110

 act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
 84
 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125

 atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
 32
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140

 gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
 80
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155 160

 aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
 28
 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

175

5

190

6

205

6

220

7

240

7

255

8

270

8

4-31452A.ST25.txt

```

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385                               390                               395                               400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                               405                               410                               415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                               420                               425                               430

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly
                               435                               440                               445

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val
                               450                               455                               460

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn
465                               470                               475                               480

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met
                               485                               490                               495

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser
                               500                               505                               510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
                               515                               520                               525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
                               530                               535                               540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545                               550                               555                               560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
                               565                               570                               575

```

Ala Gln Glu

```

<210> 7
<211> 1740
<212> DNA
<213> Artificial

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Comb
in
      ation of the mutant fiber encoded in Seq ID: #3 & 5

<220>
<221> CDS
<222> (1)..(1740)

<400> 7
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1          5          10          15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20          25          30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35          40          45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50          55          60

```


[illegible]

76

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
 12
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
 60
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
 08
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
 56
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
 04
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
 52
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
 00
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

400

cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt 15
36
Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser

510

84

525

32

540

80

560

28

575

40

<210> 8

<211> 579

<212> PRT

<213> Artificial

<400> 8

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

[illegible]

<210> 9
 <211> 1743
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acid 441(V) of wild-type fiber was deleted

<220>
 <221> CDS
 <222> (1)..(1743)

<400> 9
 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
 48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
 44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
 92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 76 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	5
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 24 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	6
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 72 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	6
210 215 220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 20 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	7
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 68 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala	7
245 250 255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val	8
260 265 270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln	8
275 280 285	

385						390						395						400	
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag																12			
48																			
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu																			
					405						410						415		
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata																12			
96																			
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile																			
					420						425						430		
ctt gct aca gtt tca gtt ttg gct aaa ggc agt ttg gct cca ata tct																13			
44																			
Leu Ala Thr Val Ser Val Leu Ala Lys Gly Ser Leu Ala Pro Ile Ser																			
					435						440						445		
gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga																13			
92																			
Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly																			
					450						455						460		
gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga																14			
40																			
Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg																			
					465						470						475		
aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt																14			
88																			
Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe																			
					485						490						495		
atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa																15			
36																			
Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys																			

4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
 40
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80

 caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
 88
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95

 ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
 36
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110

 act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
 84
 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125

 atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
 32
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140

 gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
 80
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155 160

 aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
 28
 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175

4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 76 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	5
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 24 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	6
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 72 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	6
210 215 220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 20 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	7
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 68 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala	7
245 250 255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val	8
260 265 270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln	8
275 280 285	

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
 12
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
 60
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
 08
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
 56
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
 04
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
 52
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
 00
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

580

<210> 13
 <211> 1746
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
 <221> CDS
 <222> (1)..(1746)

<220>
 <221> mutation
 <222> (1321)..(1326)

<400> 13
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 48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
 44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
 92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 76 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	5
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 24 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	6
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 72 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	6
210 215 220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 20 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	7
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 68 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala	7
245 250 255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val	8
260 265 270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln	8
275 280 285	

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
 12
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
 60
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
 08
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
 56
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
 04
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
 52
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
 00
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385	390										395			400			
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag	12																
48	Leu	Trp	Thr	Thr	Pro	Ala	Pro	Ser	Pro	Asn	Cys	Arg	Leu	Asn	Ala	Glu	
	405				410				415								
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata	12																
96	Lys	Asp	Ala	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	
	420				425				430								
ctt gct aca gtt tca gtt ttg gct gct gca ggc agt ttg gct cca ata	13																
44	Leu	Ala	Thr	Val	Ser	Val	Leu	Ala	Ala	Ala	Gly	Ser	Leu	Ala	Pro	Ile	
	435				440				445								
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat	13																
92	Ser	Gly	Thr	Val	Gln	Ser	Ala	His	Leu	Ile	Ile	Arg	Phe	Asp	Glu	Asn	
	450				455				460								
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt	14																
40	Gly	Val	Leu	Leu	Asn	Asn	Ser	Phe	Leu	Asp	Pro	Glu	Tyr	Trp	Asn	Phe	
465	470				475				480								
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga	14																
88	Arg	Asn	Gly	Asp	Leu	Thr	Glu	Gly	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gly	
	485				490				495								
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc	15																
36	Phe	Met	Pro	Asn	Leu	Ser	Ala	Tyr	Pro	Lys	Ser	His	Gly	Lys	Thr	Ala	

510

Page 60

1					5					10					15				
Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro				
			20				25						30						
Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser				
		35				40					45								
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu				
50					55					60									
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser				
65				70					75					80					
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn				
			85					90					95						
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu				
			100					105					110						
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr				
		115					120					125							
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile				
130					135					140									
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln				
145				150					155					160					
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr				
			165					170					175						
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu				
			180					185					190						
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly				

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

[illegible]

580

<210> 15
 <211> 1746
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
 <221> CDS
 <222> (1)..(1746)

<220>
 <221> mutation
 <222> (1378)..(1380)

<400> 15
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 48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
 44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
 92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 76 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	5
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 24 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	6
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 72 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	6
210 215 220	
ggg cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 20 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	7
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 68 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala	7
245 250 255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val	8
260 265 270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln	8
275 280 285	

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata gaa ttc gac gaa aat 13
92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Glu Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14
88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15
36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

4-31452A.ST25.txt

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15
84
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16
32
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16
80
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17
28
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa 17
46
Tyr Ile Ala Gln Glu

580

<210> 16
<211> 581
<212> PRT
<213> Artificial

<400> 16

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

05870261-050001

[illegible]

580

<210> 17
 <211> 1740
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 509(G) & 510(K) of wild-type fiber were deleted

<220>
 <221> CDS
 <222> (1)..(1740)

<400> 17
 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
 48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
 44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
 92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

400

500

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta 15
84
Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act 16
32
Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr

```
cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac      16
80
Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
```

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17
28
Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

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385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Thr Ala Lys Ser
500 505 510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
515 520 525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
565 570 575

Ala Gln Glu

<210> 19
 <211> 1740
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 538(G) & 539(T) of wild-type fiber were deleted

<220>
 <221> CDS
 <222> (1)..(1740)

<400> 19
 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
 48
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
 96
 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
 44
 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
 92
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

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ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
 12
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

 aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
 60
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

 gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
 08
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

 gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
 56
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

 aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
 04
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

 tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
 52
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

 agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
 00
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

400

415

430

445

460

480

495

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500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15
 84
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac cag gaa aca gga gac aca act 16
 32
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 16
 80
 Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17
 28
 Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

565

570

575

gcc caa gaa taa 17
 40
 Ala Gln Glu

<210> 20
 <211> 579
 <212> PRT
 <213> Artificial

<400> 20

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1					5					10					15				
Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro				
			20					25					30						
Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser				
		35					40					45							
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu				
	50					55					60								
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser				
65					70					75					80				
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn				
				85					90					95					
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu				
			100					105					110						
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr				
		115					120					125							
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile				
	130					135					140								
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln				
145					150					155					160				
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr				
				165					170					175					
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu				
			180					185					190						
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly				

205

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

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385                               390                               395                               400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
      405                               410                               415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
      420                               425                               430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
      435                               440                               445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
      450                               455                               460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
      465                               470                               475                               480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
      485                               490                               495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
      500                               505                               510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
      515                               520                               525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr
      530                               535                               540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
      545                               550                               555                               560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
      565                               570                               575

Ala Gln Glu

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<210> 21
<211> 38
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(38)

<400> 21
accacaccag ctccagaggc taactgtaga ctaaattgc
38

<210> 22
<211> 38
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(38)

<400> 22
gcatttagtc tacagtttagc ctctggagct ggtgtgtt
38

<210> 23
<211> 38
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(38)

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acagtttcag ttttggccgg cagtttggct ccaatatc
38
```

<210>	24
<211>	38
<212>	DNA
<213>	Artificial

<220>
<223> PCR primer

```
<220>
<221> primer_bind
<222> (1)..(38)
```

```
<400> 24
gatattggag ccaaactgcc ggccaaaact gaaactgt
38
```

<210>	25
<211>	36
<212>	DNA
<213>	Artificial

```
<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)
```

```
<400> 25
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36
```

<210>	26
<211>	36
<212>	DNA
<213>	Artificial

<220>
<223> PCR primer

<220>
 <221> primer_bind
 <222> (1)..(36)

 <400> 26
 tggagccaaa ctgccttttag ccaaaactga aactgt
 36

<210> 27
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer

<220>
 <221> primer_bind
 <222> (1)..(36)

 <400> 27
 gtttcagttt tggctgttgg cagtttggct ccaata
 36

<210> 28
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer

<220>
 <221> primer_bind
 <222> (1)..(36)

 <400> 28
 tattggagcc aaactgccaa cagccaaaac tgaaac
 36

<210> 29
 <211> 36
 <212> DNA
 <213> Artificial

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(36)

<400> 29

gtttcagttt tggctgctgc aggcagtttg gctcca
36

<210> 30

<211> 36

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(36)

<400> 30

tggagccaaa ctgcctgcag cagccaaaac tgaaac
36

<210> 31

<211> 36

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(36)

<400> 31

gctcatctta ttatagaatt cgacgaaaat ggagtg
36

<210> 32

<211> 36

<212> DNA
<213> Artificial

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)

<400> 32
cactccattt tcgtcgaatt ctataataag atgagc
36

<210> 33
<211> 39
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(39)

<400> 33
gcttatccaa aatctcacac tgccaaaagt aacattgtc
39

<210> 34
<211> 39
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(39)

<400> 34
gacaatgtta cttttggcag tgtgagattt tggataagc
39

<210>	35
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<212>	DNA
<213>	Artificial

<220>
<223> PCR primer

```
<220>
<221> primer_bind
<222> (1)..(35)
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```
<400> 35
ctaaccatta cactaaacca ggaaacagga gacac
35
```

<210>	36
<211>	35
<212>	DNA
<213>	Artificial

<220>
<223> PCR primer

```
<220>
<221> primer_bind
<222> (1)..(35)
```

```
<400> 36
gtgtctcctg tttcctgggt tagtgtaatg gttag
35
```

<210>	37
<211>	33
<212>	DNA
<213>	Artificial

<220>
<223> PCR primer

```
<220>
<221> primer_bind
<222> (1)..(33)
```

<400> 37

<210>	38
<211>	33
<212>	DNA
<213>	Artificial

```
<220>
<221> primer_bind
<222> (1)..(33)
```

<210>	39
<211>	33
<212>	DNA
<213>	Artificial

```
<220>
<221> primer_bind
<222> (1)..(33)
```

<210>	40
<211>	33
<212>	DNA
<213>	Artificial

```
<220>
<221> primer_bind
```

```
<400> 40
ggaattgttt agtaggtgtc cagtttcgtc aaa
33
```

<220>
<223> PCR primer

```
<400> 41
aacctatcag cttatgcaaa atctcacggt aaa
33
```

<220>
<223> PCR primer

```
<400> 42
tttaccgtga gattttgcat aagctgatat gt
32
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<220>
<223> cRGD consensus sequence

